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RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/10/010,731

TIME: 19:28:34

Input Set : N:\Crf3\RULE60\10010731.txt

Output Set: N:\CRF3\02142002\J010731.raw

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:

(i) APPLICANT: Liang, Jihong

Shah, Dilip Maganlal

Wu, Yonnie S.

Rosenberger, Cindy A.

Hakimi, Salim

(ii) TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold White & Durkee

(B) STREET: P.O. Box 4433

(C) CITY: Houston

(D) STATE: Texas

(E) COUNTRY: USA

(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/010,731

(B) FILING DATE: 13-Nov-2001

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/003,198

(B) FILING DATE: 07-JAN-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Patterson, Melinda L.

(B) REGISTRATION NUMBER: 33,062

(C) REFERENCE/DOCKET NUMBER: MOBT:193

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (713) 787-1400

(B) TELEFAX: (713) 787-1440

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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48   Arg Thr Cys Glu Asn Leu Ala Asp Lys Tyr Arg Gly Pro Cys Phe Ser
49   1             5             10             15
50   Gly Cys Asp Thr His Cys Thr Thr Lys Glu Asn Ala Val Ser Gly Arg
51             20             25             30
W--> 52   Cys Arg Asp Asp Phe Arg Cys Xaa Xaa Thr Lys
53             35             40
54 (2) INFORMATION FOR SEQ ID NO: 2:
55   (i) SEQUENCE CHARACTERISTICS:
56       (A) LENGTH: 45 amino acids
57       (B) TYPE: amino acid
58       (C) STRANDEDNESS:
59       (D) TOPOLOGY: linear
60   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
61   Arg Thr Cys Glu Asn Leu Ala Asp Lys Tyr Arg Gly Pro Cys Phe Ser
62   1             5             10             15
63   Gly Cys Asp Thr His Cys Thr Thr Lys Glu Asn Ala Val Ser Gly Arg
64             20             25             30
65   Cys Arg Asp Asp Phe Arg Cys Trp Cys Thr Lys Arg Cys
66             35             40             45
67 (2) INFORMATION FOR SEQ ID NO: 3:
68   (i) SEQUENCE CHARACTERISTICS:
69       (A) LENGTH: 33 base pairs
70       (B) TYPE: nucleic acid
71       (C) STRANDEDNESS: single
72       (D) TOPOLOGY: linear
73   (ix) FEATURE:
74       (A) NAME/KEY: modified_base
75       (B) LOCATION: one-of(16, 22)
76       (D) OTHER INFORMATION: /mod_base= OTHER
77 /note= "N = inosine"
78   (ix) FEATURE:
79       (A) NAME/KEY: modified_base
80       (B) LOCATION: one-of(19, 25, 28, 31)
81       (D) OTHER INFORMATION: /mod_base= OTHER
82 /note= "D = A or G or T"
83   (ix) FEATURE:
84       (A) NAME/KEY: modified_base
85       (B) LOCATION: 24
86       (D) OTHER INFORMATION: /mod_base= OTHER
87 /note= "K = G or T"
88   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89 GGAATTCGG ATCCANCADC ANCKDAADTC DTC
90 (2) INFORMATION FOR SEQ ID NO: 4:
91   (i) SEQUENCE CHARACTERISTICS:
92       (A) LENGTH: 30 base pairs
93       (B) TYPE: nucleic acid
94       (C) STRANDEDNESS: single
95       (D) TOPOLOGY: linear
96   (ix) FEATURE:

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33

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97      (A) NAME/KEY: modified_base
98      (B) LOCATION: join(18..19, 23..24, 28..29)
99      (D) OTHER INFORMATION: /mod_base= OTHER
100 /note= "N = inosine"
101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
102 GGGGAATTCGG ATCCGGGNGG GGNNGGGNNG                      30
103 (2) INFORMATION FOR SEQ ID NO: 5:
104      (i) SEQUENCE CHARACTERISTICS:
105          (A) LENGTH: 200 base pairs
106          (B) TYPE: nucleic acid
107          (C) STRANDEDNESS: double
108          (D) TOPOLOGY: linear
109      (ix) FEATURE:
110          (A) NAME/KEY: modified_base
111          (B) LOCATION: 17
112          (D) OTHER INFORMATION: /mod_base= OTHER
113 /note= "N = A or C or G or T"
114      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
115 GGGGGGGGGG GGGGGGNCAG GCTTATGCTT CCTCTCTTG GTTCTCTTTG TTGCACAAGA      60
116 AATTGTGGTG ACAGAAGCCA GAACATGTGA GAATTTGGCA GATAAATATA GGGGACCATG      120
117 CTTTAGTGGT TGTGACACTC ACTGCACAAC CAAAGAGAAC GCAGTTAGTG GAAGGTGTAG      180
118 GGACGACTTC CGCTGCTGCT                      200
119 (2) INFORMATION FOR SEQ ID NO: 6:
120      (i) SEQUENCE CHARACTERISTICS:
121          (A) LENGTH: 293 base pairs
122          (B) TYPE: nucleic acid
123          (C) STRANDEDNESS: double
124          (D) TOPOLOGY: linear
125      (ix) FEATURE:
126          (A) NAME/KEY: modified_base
127          (B) LOCATION: one-of(17, 265)
128          (D) OTHER INFORMATION: /mod_base= OTHER
129 /note= "N = A or C or G or T"
130      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
131 GGGGGGGGGG GGGGGGNTGT CAAACACACA CATAACACAT AAGTGACCGT GAGTCATTAA      60
132 ATTTATATAT ATTCATCAAT CTAATCAAAC TATGGAGAAG AAATCACTAG CTGGCTTATG      120
133 CTCCTCTTCT CTCGTTCTCT TTGTTGAACA AGAAATTATG GTGACCGAGG CAGCTACTTG      180
134 TGAGAATTTG GCTAACACAT ACAGGGGACC ATGCTTCGGT GGTGTGACT TTTACTGCAA      240
135 AACCAAAGAA CACTTACTTA GCGGNAGGTG CAGGGACGAC TTCCGCTGCT GCT          293
136 (2) INFORMATION FOR SEQ ID NO: 7:
137      (i) SEQUENCE CHARACTERISTICS:
138          (A) LENGTH: 33 base pairs
139          (B) TYPE: nucleic acid
140          (C) STRANDEDNESS: single
141          (D) TOPOLOGY: linear
142      (ix) FEATURE:
143          (A) NAME/KEY: modified_base
144          (B) LOCATION: one-of(17, 31)
145          (D) OTHER INFORMATION: /mod_base= OTHER

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146 /note= "D = A or G or T"
147     (ix) FEATURE:
148         (A) NAME/KEY: modified_base
149         (B) LOCATION: one-of(19, 20, 28)
150         (D) OTHER INFORMATION: /mod_base= OTHER
151 /note= "B = C or G or T"
152     (ix) FEATURE:
153         (A) NAME/KEY: modified_base
154         (B) LOCATION: one-of(22, 25)
155         (D) OTHER INFORMATION: /mod_base= OTHER
156 /note= "N = inosine"
157     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
158 GCGAATTCGG ATCCGADABB TNGCNGABAA DTA                      33
159 (2) INFORMATION FOR SEQ ID NO: 8:
160     (i) SEQUENCE CHARACTERISTICS:
161         (A) LENGTH: 32 base pairs
162         (B) TYPE: nucleic acid
163         (C) STRANDEDNESS: single
164         (D) TOPOLOGY: linear
165     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
166 GCGAATTCGG ATCCTTTTTT TTTTTTTTTT TT                      32
167 (2) INFORMATION FOR SEQ ID NO: 9:
168     (i) SEQUENCE CHARACTERISTICS:
169         (A) LENGTH: 327 base pairs
170         (B) TYPE: nucleic acid
171         (C) STRANDEDNESS: double
172         (D) TOPOLOGY: linear
173     (ix) FEATURE:
174         (A) NAME/KEY: modified_base
175         (B) LOCATION: one-of(244, 305)
176         (D) OTHER INFORMATION: /mod_base= OTHER
177 /note= "N = A or C or G or T"
178     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
179 GAGAATTTGG CGGATAAGTA TAGGGGACCA TGCTTTAGTG GTTGTGACAC TCACTGCACA      60
180 ACCAAAGAGA ACGCAGTTAG TGGAAGGTGT AGGGATGACT TTCGTTGTTA GTGTACTAAA      120
181 AGATGTTAAA TGGATCTCCT CCAACATCAA GATGTGCATG GAATAGTCTT TATAATAAAA      180
182 CTAAATAAAT AAAATGCACG CAGTATAGCT ACAACTTCAT CTATATATAT GTACTCAATA      240
183 TCGNGCATAA CGTATTAGTT ATGCACTTCT ATCATATGGA ATAAACATCA ATAAGTAATT      300
184 TCGTNTCCAA AAAAAAAAAA AAAAAAA                      327
185 (2) INFORMATION FOR SEQ ID NO: 10:
186     (i) SEQUENCE CHARACTERISTICS:
187         (A) LENGTH: 507 base pairs
188         (B) TYPE: nucleic acid
189         (C) STRANDEDNESS: double
190         (D) TOPOLOGY: linear
191     (ix) FEATURE:
192         (A) NAME/KEY: modified_base
193         (B) LOCATION: one-of(17, 424, 485)
194         (D) OTHER INFORMATION: /mod_base= OTHER

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195 /note= "N = A or C or G or T"

196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

197	GGGGGGGGGG	GGGGGGNTGT	CAAACACACA	CATAACACAT	AAGTGACCGT	GAGTCATTAA	60
198	ATTTATATAT	ATTCATCAAT	CTAATCAAAC	TATGGAGAAG	AAATCACTAG	CTGGCTTATG	120
199	CTTCCTCTTC	TTGGTTCTCT	TTGTTGCACA	AGAAATTGTG	GTGACAGAAG	CCAGAACATG	180
200	TGAGAATTTG	GCAGATAAAT	ATAGGGGACC	ATGCTTTAGT	GGTTGTGACA	CTCACTGCAC	240
201	AACCAAAGAG	AACGCAGTTA	GTGGAAGGTG	TAGGGACGAC	TTCCGCTGCT	GGTGACTAA	300
202	AAGATGTTAA	ATGGATCTCC	TCCAACATCA	AGATGTGCAT	GGAATAGTCT	TTATAATAAA	360
203	ACTAAATAAA	TAAAATGCAC	GCAGTATAGC	TACAACTTCA	TCTATATATA	TGACTCAATA	420
204	TCGNGCATAA	CGTATTAGTT	ATGCACTTCT	ATCATATGGA	ATAAACATCA	ATAAGTAATT	480
205	TCGTNTCCAA	AAAAAAAAAA	AAAAAAA				507

206 (2) INFORMATION FOR SEQ ID NO: 11:

207 (i) SEQUENCE CHARACTERISTICS:

208	(A) LENGTH: 62 base pairs
209	(B) TYPE: nucleic acid
210	(C) STRANDEDNESS: single
211	(D) TOPOLOGY: linear

212 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

213	GGGGATCCCA	ATCTAATCAA	ACTATGGAGA	AGAAATCACT	AGCTGGCTTA	TGCTTCCTCT	60
214	TC						62

215 (2) INFORMATION FOR SEQ ID NO: 12:

216 (i) SEQUENCE CHARACTERISTICS:

217	(A) LENGTH: 47 base pairs
218	(B) TYPE: nucleic acid
219	(C) STRANDEDNESS: single
220	(D) TOPOLOGY: linear

221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

222	GGGGATCCTT	AACATCTTTT	AGTACACCAG	CAGCGGAAGT	CGTCCCT		47
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223 (2) INFORMATION FOR SEQ ID NO: 13:

224 (i) SEQUENCE CHARACTERISTICS:

225	(A) LENGTH: 250 base pairs
226	(B) TYPE: nucleic acid
227	(C) STRANDEDNESS: double
228	(D) TOPOLOGY: linear

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

230	GGGGATCCCA	ATCTAATCAA	ACTATGGAGA	AGAAATCACT	AGCTGGCTTA	TGCTTCCTCT	60
231	TCTTGTTTCT	CTTTGTTGCA	CAAGAAATTG	TGGTGACAGA	AGCCAGAACA	TGTGAGAATT	120
232	TGGCAGATAA	ATATAGGGGA	CCATGCTTTA	GTGGTTGTGA	CACTCACTGC	ACAACCAAAG	180
233	AGAACGCAGT	TAGTGGAAGG	TGTAGGGACG	ACTTCCGCTG	CTGGTGTACT	AAAAGATGTT	240
234	AAGGATCCCC						250

235 (2) INFORMATION FOR SEQ ID NO: 14:

236 (i) SEQUENCE CHARACTERISTICS:

237	(A) LENGTH: 40 amino acids
238	(B) TYPE: amino acid
239	(C) STRANDEDNESS:
240	(D) TOPOLOGY: linear

241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

242	Ala	Thr	Cys	Glu	Asn	Leu	Ala	Asn	Thr	Tyr	Arg	Gly	Pro	Cys	Phe	Gly
243	1					5				10					15	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10010731.txt

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L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1